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RNA-seq analysis uncovers common bean genes involved in pod maturation and dehiscence

C. Gómez-Martín[1,2,*], A. González[3,*], C.R. Lebrón[1,2], C. Capel[4], F.J. Yuste-Lisbona[4], M. Hackenberg[1,2], J.L. Oliver[1,2], M. Santalla[3], **R. Lozano**[4]

[1] *Department of Genetics, Faculty of Science, University of Granada, Granada, Spain*
[2] *Laboratory of Bioinformatics, Centro de Investigación Biomédica, Granada, Spain*
[3] *Grupo de Biología de Agrosistemas, Misión Biológica de Galicia-CSIC, Pontevedra, Spain*
[4] *Centro de Investigación en Biotecnología Agroalimentaria (CIAIMBITAL), Universidad de Almeria, Almeria, Spain*

** Both authors contributed equally to this work*

Fruit maturation and dehiscence are important developmental processes in legume species as they influence fruit quality and crop productivity (Tang et al., 2013). Despite that key regulators of fruit development have been characterized in the model species *Arabidopsis thaliana*, the genetic basis of fruit maturation and dehiscence remains unknown in agricultural species like common bean (Li and Olsen, 2016). Recent advances in genetic, molecular and physiological research, mostly brought about by the implementation of high-throughput and next generation sequencing (NGS) technologies have begun to decipher the genetic networks regulating fruit development. With the aim to unravel the transcriptomic changes associated to pod maturation and dehiscence, we used a powerful RNA-seq bioinformatics protocol to compared immature and mature pods of two accessions, which also differed in deshiscence and fiber content. RNA-seq short reads were aligned to the most recent update of the *Phaseolus vulgaris* reference genome, then computing the fold changes in assembled transcript expression among different developmental stages. Using *Phytozome* gene annotation for common bean, a significant number of differentially expressed genes (DEGs) were associated with pod maturation in both accessions, which were mainly involved in transmembrane transporter activity, carbohydrate metabolism and photosynthesis. Furthermore, among DEGs between dehiscent and indehiscent fruits highlights genes related to oxidation-reduction and lipid metabolic processes. This work provides comprehensive insights into pod maturation and dehiscence, identifying gene expression profiles with major roles on these developmental processes.

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